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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=10; day=15; hr=11; min=45; sec=54; ms=572; ]

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Reviewer Comments:

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<110> FirstName : Thomas  
<110> MiddleInitial :  
<110> Suffix :

Please do not submit a PatentIn "prj" file. It is "work-in-progress" file only; you will need to submit a generated Sequence listing. To generate one, go to "Application Steps" on PatentIn main menu. Clic on "Generate Sequence Listing" and the click "Start" button. PatentIn will validate each sequence, hopefully you will see "Successful completion" in the white box above the "Start" button.

You can then view teh generated Sequence Listing by going to "Project" on main menu, and clicking on view/Print Sequence listing. A generated PatentIn Sequence Listing will have an "ST25" file extention.

For further assistance, please contact Mark Spencer at 571-272-2510

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Application No: 10078927

Version No: 5.0

**Input Set:****Output Set:****Started:** 2008-09-10 14:26:10.607**Finished:** 2008-09-10 14:26:20.340**Elapsed:** 0 hr(s) 0 min(s) 9 sec(s) 733 ms**Total Warnings:** 59**Total Errors:** 35**No. of SeqIDs Defined:** 0**Actual SeqID Count:** 0

Error code	Error Description
E 248	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
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E 248	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
E 248	Order Sequence Error <141> -> <213>; Expected Mandatory Tag: <210> in Header
W 402	Undefined organism found in <213> in Seq ID (0)
E 202	Invalid input format; Value must be an integer in <400> SeqID: (0)
W 112	Upper case found in data; Found at position(0) SeqId(0)
W 112	Upper case found in data; Found at position(1) SeqId(0)

**Input Set:**

**Output Set:**

**Started:** 2008-09-10 14:26:10.607  
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Error code	Error Description
W 112	Upper case found in data; Found at position(2) SeqId(0)
W 112	Upper case found in data; Found at position(3) SeqId(0)
W 112	Upper case found in data; Found at position(4) SeqId(0)
W 112	Upper case found in data; Found at position(5) SeqId(0)
E 310	Invalid sequence type in <212> in SEQID: (0)
E 248	Order Sequence Error <212> -> <211>; Expected Mandatory Tag: <213> in Header
E 202	Invalid input format; Value must be an integer in <211> in SEQ ID
E 248	Order Sequence Error <211> -> <221>; Expected Mandatory Tag: <212> in Header
E 257	Invalid sequence data feature in <221> in SEQ ID (0)
W 401	Unrecognized range formatin <222> in SEQID (0)
W 401	Unrecognized range formatin <222> in SEQID (0)
E 257	Invalid sequence data feature in <221> in SEQ ID (0)
W 401	Unrecognized range formatin <222> in SEQID (0)
W 401	Unrecognized range formatin <222> in SEQID (0)
E 248	Order Sequence Error <222> -> <213>; Expected Mandatory Tag: <400> in Header
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W 112	Upper case found in data; Found at position(5) SeqId(0)
W 112	Upper case found in data; Found at position(6) SeqId(0)
W 112	Upper case found in data; Found at position(7) SeqId(0)
W 112	Upper case found in data; Found at position(8) SeqId(0)
W 112	Upper case found in data; Found at position(9) SeqId(0)
W 112	Upper case found in data; Found at position(10) SeqId(0)
W 112	Upper case found in data; Found at position(11) SeqId(0)
W 112	Upper case found in data; Found at position(12) SeqId(0)
W 112	Upper case found in data; Found at position(13) SeqId(0) This error has occurred more than 20 times, will not be displayed
E 310	Invalid sequence type in <212> in SEQID: (0)
E 248	Order Sequence Error <212> -> <211>; Expected Mandatory Tag: <213> in Header
E 202	Invalid input format; Value must be an integer in <211> in SEQ ID
E 248	Order Sequence Error <211> -> <221>; Expected Mandatory Tag: <212> in Header
E 257	Invalid sequence data feature in <221> in SEQ ID (0)
W 401	Unrecognized range format in <222> in SEQID (0)
W 401	Unrecognized range format in <222> in SEQID (0)
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W 401	Unrecognized range format in <222> in SEQID (0)
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E 248	Order Sequence Error <222> -> <213>; Expected Mandatory Tag: <400>

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E 257	Invalid sequence data feature in <221> in SEQ ID (0)
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Application Project

-----  
<120> Title : Cyclin Dependent Kinase 5 Phosphorylation of Disabled 1 Protein

<130> AppFileReference : SJ-01-0032  
<140> CurrentApplNumber : 10/078,927  
<141> CurrentFilingDate : 2002-02-19

#### Sequence

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<213> OrganismName : Mus musculus

<400> PreSequenceString :

QSSPSK

6

<212> Type : PRT

<211> Length : 6

SequenceName : Seq ID#1

SequenceDescription :

#### Feature

-----

Sequence: Seq ID#1:

<221> FeatureKey : SITE

<222> LocationFrom : 3

<222> LocationTo : 3

Other Information : Serine at residue #3 equates to Serine491 in mouse Dab1 sequence

Cdk5 phosphorylation of Serine requires a Proline (P) in the +1 position and a Lysine (K) in the +3 position

CDSJoin : No

#### Feature

-----

Sequence: Seq ID#1:

<221> FeatureKey : DOMAIN

<222> LocationFrom : 1

<222> LocationTo : 6

Other Information : smallest carboxy terminal Dab1 tryptic fragment containing a Cdk5 phosphorylation site

CDSJoin : No

#### Sequence

-----

<213> OrganismName : Mus musculus

<400> PreSequenceString :

SSASHVSDPT ADDIFEEGFE SPSK

24

<212> Type : PRT

<211> Length : 24

SequenceName : Seq ID#2

SequenceDescription :

#### Feature

-----

Sequence: Seq ID#2:

<221> FeatureKey : SITE

<222> LocationFrom : 21

<222> LocationTo : 21

Other Information : Serine at Residue 21 equates to Serine515 in mouse Dab1 sequence

Cdk5 phosphorylation of Serine requires a Proline (P) in the +1 position and a Lysine (K) in the +3 position

CDSJoin : No



Feature

-----

Sequence: Seq ID#2:

<221> FeatureKey : DOMAIN

<222> LocationFrom : 1

<222> LocationTo : 24

Other Information : Dab1 tryptic fragment containing a Cdk5 phosphorylation site  
CDSJoin : No

Sequence

-----

<213> OrganismName : Mus musculus

<400> PreSequenceString :

TPAPRQSSPS KSSA

14

<212> Type : PRT

<211> Length : 14

SequenceName : Seq ID#3

SequenceDescription :

Feature

-----

Sequence: Seq ID#3:

<221> FeatureKey : MOD\_RES

<222> LocationFrom : 8

<222> LocationTo : 8

Other Information : PHOSPHORYLATION, equates to Serine491 in mouse Dab1 sequence

Cdk5 phosphorylation of Serine requires a Proline (P) in the +1 position and a Lysine (K) in the +3 position

CDSJoin : No

Feature

-----

Sequence: Seq ID#3:

<221> FeatureKey : DOMAIN

<222> LocationFrom : 1

<222> LocationTo : 14

Other Information : Dab1 phosphopeptide domain used for antibody production

CDSJoin : No